

1 CACAGACAGGGCTCTTAACGTGTTATATCACTCACTGGGAAAGTGTCTCAAGCTGTTCTA
61 CAAATCCATGCAAAGGCCGTTAAAAATAGCAGCGAAGGTCTGGACTCGGTCTCGTCCA
121 GCACAGCCCCCTGGCTCTCTCTGGGCTCTGGCCGCCTGGCCCCCGGGGACCCACACGA
181 GGTCATGGCGTGCTTCGGCAGGGGGGGGGATCCCATAAGACACCTCAGCTCCTTAAGA
241 GTTCTCCGCCTGGGCCAGGACGAGCATGGGGTCCCCACTGATGCCGAGACAGTGCCCC
301 TGTGTGTGTGAGCCCTCGACCCACATAACAGAGAGGTGTCCTGATGCCCTGTGCTCTC
361 CAGGTGGATCTAGGATCCGGCTTCAAACATGTGGCAGCTCTGGCCTCCCTGCTGCCT
421 GCTGGTGTGGCAATGCCCGGAGCAGGCCCTTTCCATCCGTGTCGGATGAGCTGGT
481 CAACTATGTCAACAAACGGAATACCACGTGGCAGGCCGGCACAACTTCTACAACGTGGA
541 CATGAGCTACTTGAAGAGGGTATGTGGTACCTTCTGGTGGGCCAAGCCACCCAGAG
601 AGTTATGTTACCGAGGACCTGAAGCTGCCTGCAAGCTTCGATGCACGGAACAAATGGCC
661 ACAGTGTCCCACCATCAAAGAGATCAGAGACCAGGGCTCCTGTGGCCTGCTGGTAAG
721 GCCCTGCTGGCTGGTGGGAAGCGCTGGAGAGAAAGTGGAGCAACACTGGAGAGTCTTG
781 GGGGATTCGGGGTGGGACAACCTTGACAAGGCAAGTTATAGAAACTTCTGAGTCCCAG
781 TTTCCATCAGTACAAAATACAATCCCTCTGCCATGAATGATGGCGAGGATTAGGTGG
841 AGTGGCGGGCAGAGCATCCAGCAGATTGCAAGTCCACGTGTACAGGTGGCGAACAGCTC
901 CCTTTCCCTGACATGCTGGCCCGTCCGCAAATACCAGGAGCTCTACTGCTACTCTGCTT
961 CAAGAAAGCATCCCTTAGTGTCAAGTGTCTTAATTTCATTTAATTGTGGTAA
1021 AATACACGTAACAGAAATGTAATAATCTTAGCAATCTCTTTGTTTCTTTCTTTT
1081 TTTTTTTTTTTTTTT

FIGURE 1

1 MWQLWASLCCLLVLANARSRPSFHPVSDELVNYVNKRNTTWQAGHNFYNVDMMSYLKRLCG
61 TFLGGPKPPQRVMFTEDLKLPAFDAREQWPQCPTIKEIRDQGSCGSCWVRPCWLVGKRW
121 RESGSNTGESWGIRGGDNSDKASYRNFLSPSFHQYKNHNPSGHE

FIGURE 2

1 TCCAAGTCCTGGATGAGCTCGGAAGACACGTGCTGCGGAAGGACTGTGGCCCAGTGG
61 ACACCAAGGTTCCAGGTGCTGGGAGCCCAAGTCAGCCTCACTCAGGGCTCAGCCATGA
121 TTTCTTCTGTCCCCAAAACCATCCAGACAACAGAAACGAGACTTTCAGCTCAGTCATT
181 CCCTGTTGAATGAGGATCCCTGTCCCAGGACTTGCTGTGAAGATGGCTCAATCTCA
241 AGAACTTTGTCATTACCTATAACCGGACATATGAGTCAAAGGAAGAAGCCCGTGGCGCC
301 TGTCCGTCTTGTCAATAACATGGTGCAGCACAGAAGATCCAGGCCCTGGACCGTGGCA
361 CAGCTCAGTATGGAGTCACCAAGTTCACTGATCTCACAGAGGAGGAGTTCCGCACTATCT
421 ACCTGAATACTCTCCTGAGGAAAGAGCCTGGCAACAAAGATGAAGCAAGCCAAGTCTGTGG
481 GTGACCTCGCCCCACCTGAATGGACTGGAGGAGTAAGGGGCTGTCAACAAAGTCAAAG
541 ACCAGGGCATGTGTGGCTCCTGCTGGCCCTCTCAGTCACAGGCAATGTGGAGGGCCAGT
601 GGTTTCTCAACCAGGGACCCCTGCTCCCTCTGAACAGGAGCTTGGACTGTGACA
661 AGATGGACAAGGCCTGCATGGCGGCTTGCCTCCAATGCCTACTCGGCCATAAAGAATT
721 TGGGAGGGCTGGAGACAGAGGATGACTACAGTACCGGTACATGCAGTCCTGCAACT
781 TCTCAGCAGAGAACGCCAAGGTCTACATCAATGACTCCGTGGAGCTGAGCCAGAACGAGC
841 AGAAGCTGGCAGCCTGGCTGCCAAGAGAGGCCAATCTCCGTGGCCATCAATGCCTTG
901 GCATGCAGTTTACCGCCACGGGATCTCCGCCCTCTCCGGCCCTCTGCAGCCCTGGC
961 TCATTGACCATGCGGTGTTGCTTGTGGCTACGGCAACCGCTCTGACGTTCCCTTGGG
1021 CCATCAAGAACAGCTGGGCACTGACTGGGTGAGAACGGTTACTACTACTTGATCGCG
1081 GGTCCGGGCCTGTGGCGTGAACACCATGGCCAGCTCGCGGTGGACTGAAGAGGGG
1141 CCCCCAGCTGGGACCTGGTGTGATCAGAGTGGCTGCTGCCCAAGCCTGACATGTGTCC
1201 AGGCCCTCCCCGGGAGGTACAGCTGGCAGAGGAAAGGCACTGGTACCTCAGGGTGAG
1261 CAGAGGGCACTGGCTGGGACAGCCCTGCTT

FIGURE 3

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1 MISSLSQNHPDNRNETFSSVISLLNEDPLSQDLPVKMASIFKNFVITYNRRTYESKEEARW
61 RLSVFVNMMVRAQKIQALDRGTAQYGVTKFSDLTEEFRTIYLNTLLRKEPGNKMHQAKS
121 VGD LAPPEWDWRSKGAVTKV DQGMCGSCWAFSVTGNVEGQWFLNQGTLLSLSEQELLDC
181 DKMDKACMGGLPSNAYS A I KNLGGLETEDDY SY QGHMQSCNFSAEKAKVYINDSVELSQN
241 EQKLAALWLA RGPI SVAINA FG MQFYRH G ISRPLRPLCSPWLIDHAVLLVG YGNRSDVPF
301 WAIKNSWGT DWGEK GYYYLHRGSGACGVNTMASSAVVD

FIGURE 4

1 atgtcgtgcg tcaagttatg gcccagcggt gccccggcc ccttggtgtc catcgaggaa
61 ctggagaacc aggagctcgt cggcaaagac gggttcggca cagtgttccg ggcgcaacat
121 aggaagtggg gctacgatgt ggccggtaag atcgtaaact cgaaggcgat atccagggag
181 gtcaaggcca tggcaagtct ggataacgaa ttcgtgttgc gcctagaagg gtttatcgag
241 aaggtaact gggaccaaga tcccaagccg gctctggta ctaaattcat ggagaacggc
301 tccctgtcgg ggctgctgca gtcccagtgc cctcggccct ggccgctcct ttgccgcctg
361 ctgaaagaag tggtgcttgg gatgtttac ctgcacgacc agaaccggg gtcctgcac
421 cgggacctca agccatccaa cgtcctgccc gacccagagc tgcacgtcaa gctggcagat
481 tttggcctgt ccacattca gggaggctca cagtcaggga cagggtccgg ggagccaggg
541 ggcaccctgg gctacttggc cccagaactg tttgttaacg taaaccggaa ggcctccaca
601 gccagtgacg tctacagctt cgggatccta atgtggcag tgcttgctgg aagagaagtt
661 gagttgccaa ccgaaccatc actcgtgtac gaagcagtgt gcaacaggca gaaccggcct
721 tcattggctg agctgcccc agccggcct gagactccg gcttagaagg actgaaggag
781 ctaatgcagc tctgctggag cagtgagccc aaggacagac ctccttcca ggaatgccta
841 ccaaaaactg atgaagtctt ccagatggtg gagaacaata tgaatgctgc tgtctccacg
901 gtaaaggatt tcctgtctca gctcaagagc agcaatagga gatTTCTAT cccagagtca
961 ggccaaggag ggacagaaaat ggatggctt aggagaacca tagaaaacca gcactctcgt
1021 aatgatgtca tggtttctga gtggctaaac aaactgaatc tagaggagcc tcccagctct
1081 gttcctaaaa aatgcccagag ctttaccaag aggagcaggg cacaagagga gcaggttcca
1141 caaggctgga cagcaggcac atcttcagat tcgatggccc aacccccc gactccagag
1201 acctcaactt tcagaaacca gatgcccagc cctacctcaa ctggaacacc aagtccctgga
1261 ccccgaggga atcagggggc tgagagacaa ggcattgaact ggtcctgcag gacccggag
1321 ccaaattccag taacagggcg accgctcggt aacatataca actgctctgg ggtgcaagtt
1381 ggagacaaca actacttgac tatgcaacag acaactgcct tgcccacatg gggcttggca
1441 cttcgggca aggggagggg cttgcagcac ccccccaccag tagttcgca agaaggccct
1501 aaagatcctg aagcctggag caggccacag ggttggtata atcatagcgg gaaataa

FIGURE 5

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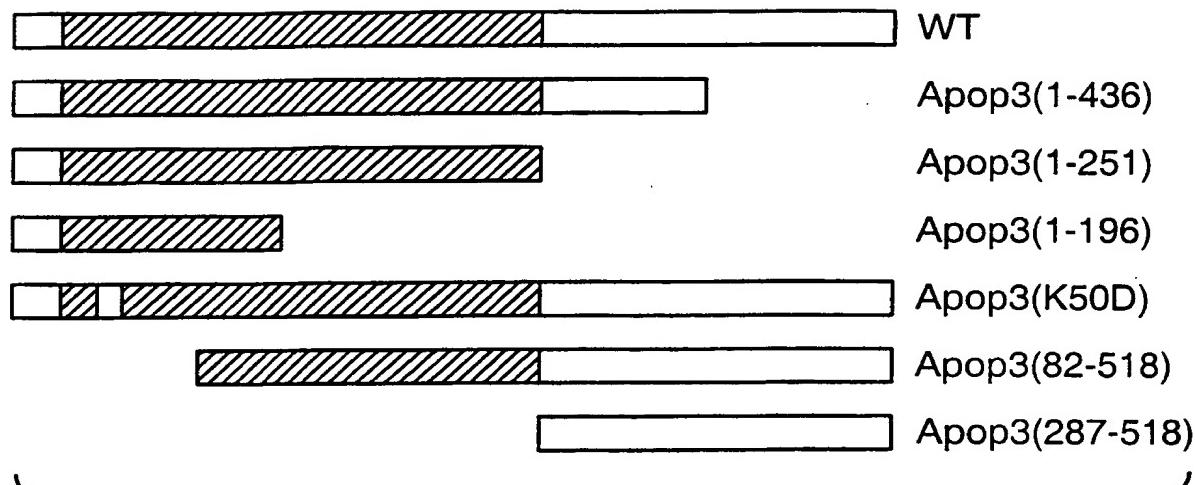
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1 MSCVKLWPSGAPAPLVSIEELENQELVGKDGFGTVFRAQHRKWGYDVAVKIVNSKAISRE
61 VKAMASLDNEFVLRLEGVIEKVNWQDQDPKPALVTKFMEENGSLSGLLQSQCPRPWPLLCL
121 LKEVVLGMFYLHDQNPVLLHRDLKPSNVLPDPELHVKLADFGLSTFQGGSQSGTGSGEPG
181 GTLGYLAPELFVNVRKASTASDVYSGILMWAVLAGREVELPTEPSLVYEAVCNRQNRP
241 SLAELPQAGPETPGLEGLKELMQLCWSSEPKDRPSFQECLPKTDEVFQMVENNMNAAVST
301 VKDFLSQLKSSNRRFSIPESGQGGTEMDGFRRTIENQHSRNDVMVSEWLKNLNLEEPSS
361 VPKKCPSLTKRSRAQEEQVPQAWTAGTSSDSMAQPPQTETSTFRNQMPSPSTGTPTSPG
421 PRGNQGAERQGMNWSCRTPEPNPVTGRPLVNIYNCGVQVGDNNYLTMQTTALPTWGLA
481 PSGKGRGLQHPPPVGSQEGPKDPEAWSRPQGWYNHSGKZ

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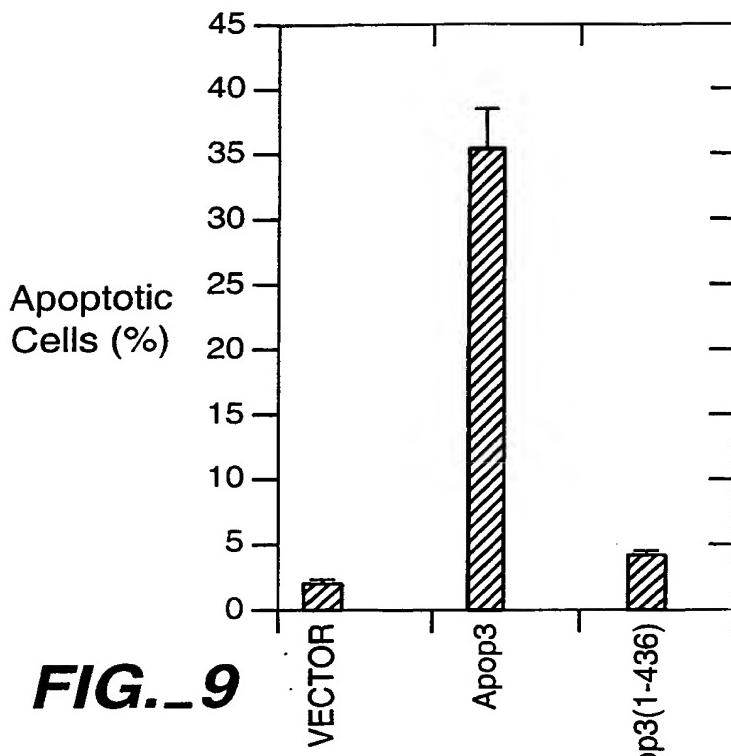
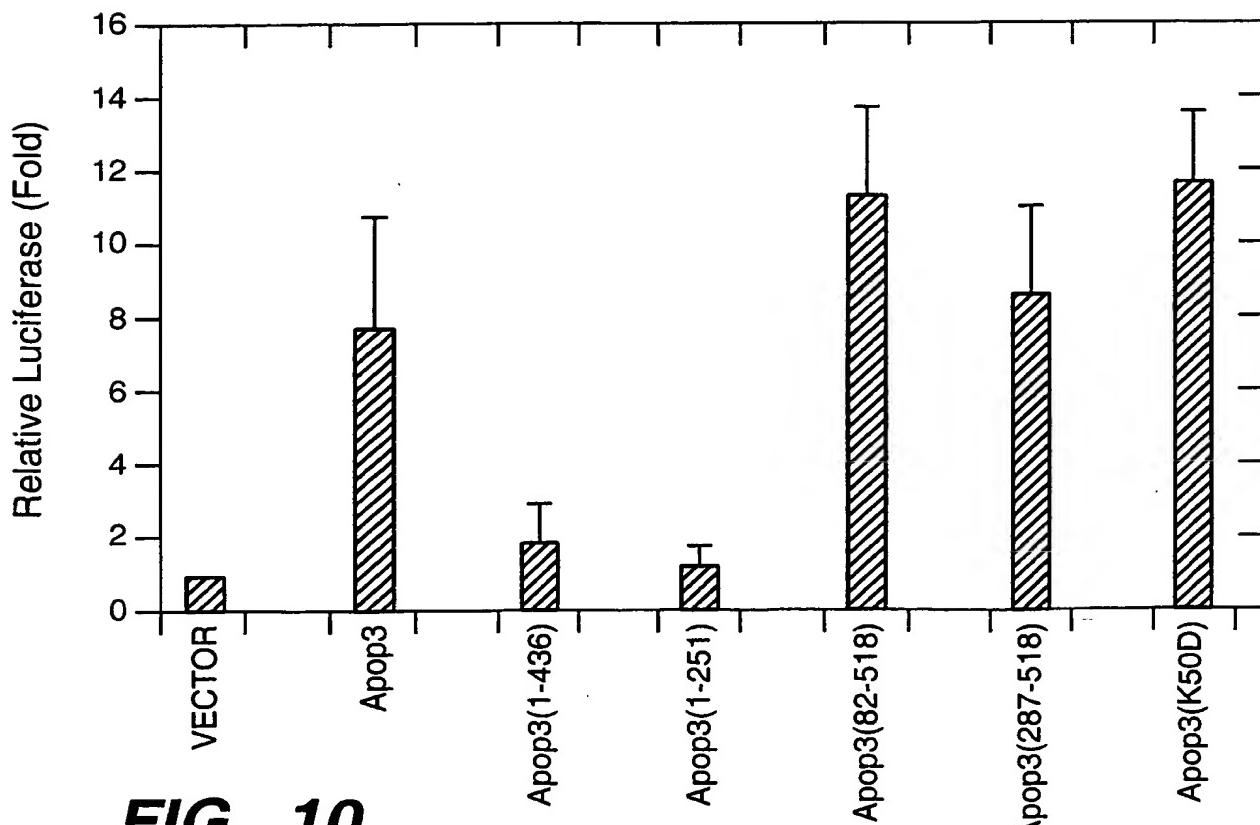
FIGURE 6

***FIG._7***

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FIG._8

Binding To RIP	
Apop3	++++
Apop3(1-436)	+
Apop3(1-251)	-
Apop3(1-196)	-
Apop3(K50D)	++++
Apop3(82-518)	+++
Apop3(287-518)	-

**FIG._9****FIG._10**